

1. *Chlorophyll* (green)
 2. *Carotenoids* (yellow, orange, red)
 3. *Xanthophylls* (yellow)
 4. *Lutein* (yellow)
 5. *Zeaxanthin* (yellow)
 6. *Anthoxanthins* (white)
 7. *Anthocyanins* (red, purple, blue)
 8. *Flavonols* (yellow, orange)
 9. *Flavones* (yellow)
 10. *Flavonols* (yellow, orange)
 11. *Flavones* (yellow)
 12. *Flavonols* (yellow, orange)
 13. *Flavones* (yellow)
 14. *Flavonols* (yellow, orange)
 15. *Flavones* (yellow)
 16. *Flavonols* (yellow, orange)
 17. *Flavones* (yellow)
 18. *Flavonols* (yellow, orange)
 19. *Flavones* (yellow)
 20. *Flavonols* (yellow, orange)

[illegible]

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAATEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGKWHLGFNKKEC
MPTRRGFDFTFFGSLLGSGDYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNSSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

[illegible]

CGGACGCGTGGGTGCGAGTGGAGCGGAGCCCGAGCGGCTGAGGAGAGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTTCGGGAACGCGGCCAGTGC AAGGCATCACGGGTGTTAGCATCGGCACGT CAGCCT
GGGGTCTGTCACTATGGAAC TAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGT AAGTTTGGTGAGTGC GTGGGACCAAACAAAT
GCAGATGCTTTCCAGGATACACCGGGA AAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCCT
CAGTGGCCACATGCTCATGCCAGATGTCTACGTGTGTGA ACTCTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAGGGCCACAGTGCCCTGTGTCCATCCTCAGGA
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTTGAAGCTACTACTGCAAATGT CACA
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TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAGAACCCACCAGGACTCC
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AAGGTGAATGAAGCAGGTGAATTTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGTTGACTGCGAGCTTCAATCATGGGATCTGTGACT
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CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTTCGGGAAACTTCGAGTGTTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATT CAGTTGTATCAAGGAACTGATGC
TACCAAAGCATCATTTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCAAAATCGCAGTGG
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TTACTATCTTTATATTTGACTTTTGTATGT CAGTTCCTGGTTTTTTTTTGATATGTCATAG
GACCTCTGGCATTTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCTTTCTTGATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA
AACTATGACATCAAAGATAGACTTTTTGCCTAAGTGGCCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAAATCTTTTGTAATAATAA